

SEQUENCE LISTING

<110> Elbaz, Nathalie
Nahmias, Clara
Strosberg, Arthur Donny

<120> NUCLEIC SEQUENCES ENCODING AN AT2
RECEPTOR-INTERACTING PROTEIN (ATIP) AND THEIR APPLICATIONS

<130> 33339/208804

<140> US 09/762,194

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<150> PCT/FR99/01908

<151> 1999-08-02

<150> FR 98/09997

<151> 1998-08-04

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1803

<212> DNA

<213> Mus musculus

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<221> CDS

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gcc aaa gga	ctg ctt cga	aac ctc cgg	ctt cct tcg	ggg ctc agg	aaa	276
Ala Lys Gly	Leu Leu Arg	Asn Leu Arg	Leu Pro Ser	Gly Leu Arg	Lys	
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aac act gtc	att ttc cac	aca gtt gaa	aag ggc agg	cag aag aat	ccc	324
Asn Thr Val	Ile Phe His	Thr Val Glu	Lys Gly Arg	Gln Lys Asn	Pro	

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Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser Ser			
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gag aga acg ctt gag ttg gcc caa tac aag aca aaa tgt gaa agc caa			420
Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser Gln			
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agt gga ttc atc ctg cac ctc agg cag ctt ctt tcc cgt ggt aac aac			468
Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn Asn			
85	90		95
aag ttt gaa gcg ctg aca gtt gtg atc cag cac ctc ctg tct gag cgg			516
Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu Arg			
100	105		110
gag gaa gca ctg aag caa cac aaa acc ctc tct caa gaa ctt gtc agc			564
Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val Ser			
115	120		125
ctc cgg gga gag cta gtt gct gct tca agc gcc tgt gag aag cta gaa			612
Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu Glu			
130	135		145
aag gct agg gct gac tta cag aca gcg tat caa gaa ttt gtc cag aaa			660
Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln Lys			
150	155		160
cta aac cag cag cat cag aca gac cgg acg gaa ctg gag aac cgg ctg			708
Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu			
165	170		175
aag gac tta tac acc gca gag tgt gag aag ctt cag agc att tac att			756
Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile			
180	185		190
gag gag gca gaa aaa tat aaa act caa ctg caa gag cag ttt gac aac			804
Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn			
195	200		205
tta aac gcc gcc cat gag acc act aag ctt gag att gaa gct agc cac			852
Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His			
210	215		225
tcg gag aag gtg gaa ttg ctg aag aag acc tat gaa acc tcc ctt tca			900
Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser			
230	235		240
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Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu			
245	250		255

ctt aat gag aag cag gaa tcg ctg gag aaa caa atc aat gat ctg aag	996
Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys	
260 265 270	
agt gaa aac gat gct tta aac gaa agg ttg aaa tca gag gag caa aag	1044
Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln Lys	
275 280 285	
caa ctg tca aga gag aag gcg aat tcc aaa aac cct cag gtc atg tat	1092
Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met Tyr	
290 295 300 305	
ctg gag caa gaa cta gaa agc ctg aag gct gtg tta gag atc aag aat	1140
Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn	
310 315 320	
gag aag ctg cac cag cag gac atg aag cta atg aag atg gaa aag ctg	1188
Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys Leu	
325 330 335	
gtg gac aat aac aca gca ttg gtt gac aag ctg aag cga ttc cag cag	1236
Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln	
340 345 350	
gaa aac gag gag tta aaa gct cgc atg gac aaa cac atg gca att tca	1284
Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile Ser	
355 360 365	
agg caa ctt tcc acc gag cag gcc gcg ctg caa gag tcc ctt gag aag	1332
Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu Lys	
370 375 380 385	
gag tca aag gtc aac aag aga ctg tcc atg gag aac gag gaa ctt ctg	1380
Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu Leu	
390 395 400	
tgg aaa ctg cac aac gga gac ctg tgc agc ccc aag aga tcc ccc acc	1428
Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro Thr	
405 410 415	
tcc tcg gcc atc cct ttc cag tcc ccc agg aat tct ggt tcc ttc tcc	1476
Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe Ser	
420 425 430	
agc ccc agc atc tca ccc aga tga cggcttctga acgcaggaga ctctctgaag	1530
Ser Pro Ser Ile Ser Pro Arg *	
435 440	
gcactgaggt gcgcttctgc aggactgacc ctctcatggg aactcgagtt gctgcgttag	1590
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aatagagagc tccaatagaa gacttttaac ttggtccaaa agcctcctcc aaaaacagat	1710
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1803

<210> 2

<211> 440

<212> PRT

<213> Mus musculus

<400> 2

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			20					25					30		
Lys	Asn	Thr	Val	Ile	Phe	His	Thr	Val	Glu	Lys	Gly	Arg	Gln	Lys	Asn
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Pro	Arg	Ser	Leu	Cys	Ile	Gln	Thr	Gln	Thr	Ala	Pro	Asp	Val	Leu	Ser
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Ser	Glu	Arg	Thr	Leu	Glu	Leu	Ala	Gln	Tyr	Lys	Thr	Lys	Cys	Glu	Ser
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Gln	Ser	Gly	Phe	Ile	Leu	His	Leu	Arg	Gln	Leu	Leu	Ser	Arg	Gly	Asn
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Asn	Lys	Phe	Glu	Ala	Leu	Thr	Val	Val	Ile	Gln	His	Leu	Leu	Ser	Glu
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Arg	Glu	Glu	Ala	Leu	Lys	Gln	His	Lys	Thr	Leu	Ser	Gln	Glu	Leu	Val
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Ser	Leu	Arg	Gly	Glu	Leu	Val	Ala	Ala	Ser	Ser	Ala	Cys	Glu	Lys	Leu
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Lys	Leu	Asn	Gln	Gln	His	Gln	Thr	Asp	Arg	Thr	Glu	Leu	Glu	Asn	Arg
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Leu	Lys	Asp	Leu	Tyr	Thr	Ala	Glu	Cys	Glu	Lys	Leu	Gln	Ser	Ile	Tyr
		180					185					190			
Ile	Glu	Glu	Ala	Glu	Lys	Tyr	Lys	Thr	Gln	Leu	Gln	Glu	Gln	Phe	Asp
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Asn	Leu	Asn	Ala	Ala	His	Glu	Thr	Thr	Lys	Leu	Glu	Ile	Glu	Ala	Ser
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His	Ser	Glu	Lys	Val	Glu	Leu	Leu	Lys	Lys	Thr	Tyr	Glu	Thr	Ser	Leu
225				230					235					240	
Ser	Glu	Ile	Lys	Lys	Ser	His	Glu	Met	Glu	Lys	Lys	Ser	Leu	Glu	Asp
			245					250					255		
Leu	Leu	Asn	Glu	Lys	Gln	Glu	Ser	Leu	Glu	Lys	Gln	Ile	Asn	Asp	Leu
		260					265					270			
Lys	Ser	Glu	Asn	Asp	Ala	Leu	Asn	Glu	Arg	Leu	Lys	Ser	Glu	Glu	Gln
	275						280					285			
Lys	Gln	Leu	Ser	Arg	Glu	Lys	Ala	Asn	Ser	Lys	Asn	Pro	Gln	Val	Met
	290					295					300				
Tyr	Leu	Glu	Gln	Glu	Leu	Glu	Ser	Leu	Lys	Ala	Val	Leu	Glu	Ile	Lys
305				310					315					320	
Asn	Glu	Lys	Leu	His	Gln	Gln	Asp	Met	Lys	Leu	Met	Lys	Met	Glu	Lys
			325					330					335		
Leu	Val	Asp	Asn	Asn	Thr	Ala	Leu	Val	Asp	Lys	Leu	Lys	Arg	Phe	Gln
		340					345						350		
Gln	Glu	Asn	Glu	Glu	Leu	Lys	Ala	Arg	Met	Asp	Lys	His	Met	Ala	Ile

355	360	365
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370	375	380
Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu		
385	390	395
Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro		400
405	410	415
Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe		
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Ser Ser Pro Ser Ile Ser Pro Arg		
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<220>
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acc gcc aaa gga ctg ctt cga aac ctc cgg ctt cct tcg ggg ctc agg	96
Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg	
20 25 30	
aaa aac act gtc att ttc cac aca gtt gaa aag ggc agg cag aag aat	144
Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn	
35 40 45	
ccc agg agc ctg tgc atc cag acc cag aca gct cca gat gtg ctg tcc	192
Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser	
50 55 60	
tcc gag aga acg ctt gag ttg gcc caa tac aag aca aaa tgt gaa agc	240
Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser	
65 70 75 80	
caa agt gga ttc atc ctg cac ctc agg cag ctt ctt tcc cgt ggt aac	288
Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn	
85 90 95	
aac aag ttt gaa gcg ctg aca gtt gtg atc cag cac ctc ctg tct gag	336
Asn Lys Phe Glu Ala Leu Thr Val Ile Gln His Leu Leu Ser Glu	
100 105 110	
cgg gag gaa gca ctg aag caa cac aaa acc ctc tct caa gaa ctt gtc	384
Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val	
115 120 125	

agc ctc cgg gga gag cta gtt gct gct tca agc gcc tgt gag aag cta	432
Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu	
130 135 140	
 gaa aag gct agg gct gac tta cag aca gcg tat caa gaa ttt gtc cag	480
Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln	
145 150 155 160	
 aaa cta aac cag cag cat cag aca gac cgg acg gaa ctg gag aac cgg	528
Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg	
165 170 175	
 ctg aag gac tta tac acc gca gag tgt gag aag ctt cag agc att tac	576
Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr	
180 185 190	
 att gag gag gca gaa aaa tat aaa act caa ctg caa gag cag ttt gac	624
Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp	
195 200 205	
 aac tta aac gcc gcc cat gag acc act aag ctt gag att gaa gct agc	672
Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser	
210 215 220	
 cac tcg gag aag gtg gaa ttg ctg aag aag acc tat gaa acc tcc ctt	720
His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu	
225 230 235 240	
 tca gaa atc aag aag agc cat gag atg gag aag aag tca ctg gag gat	768
Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp	
245 250 255	
 ctg ctt aat gag aag cag gaa tcg ctg gag aaa caa atc aat gat ctg	816
Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu	
260 265 270	
 aag agt gaa aac gat gct tta aac gaa agg ttg aaa tca gag gag caa	864
Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln	
275 280 285	
 aag caa ctg tca aga gag aag gcg aat tcc aaa aac cct cag gtc atg	912
Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met	
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 tat ctg gag caa gaa cta gaa agc ctg aag gct gtg tta gag atc aag	960
Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys	
305 310 315 320	
 aat gag aag ctg cac cag cag gac atg aag cta atg aag atg gaa aag	1008
Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys	
325 330 335	

ctg gtg gac aat aac aca gca ttg gtt gac aag ctg aag cga ttc cag	1056
Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln	
340 345 350	
cag gaa aac gag gag tta aaa gct cgc atg gac aaa cac atg gca att	1104
Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile	
355 360 365	
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Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu	
370 375 380	
aag gag tca aag gtc aac aag aga ctg tcc atg gag aac gag gaa ctt	1200
Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu	
385 390 395 400	
ctg tgg aaa ctg cac aac gga gac ctg tgc agc ccc aag aga tcc ccc	1248
Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro	
405 410 415	
acc tcc tcg gcc atc cct ttc cag tcc ccc agg aat tct ggt tcc ttc	1296
Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe	
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<212> PRT

<213> Mus musculus

<400> 4

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Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn	
35 40 45	
Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser	
50 55 60	
Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser	
65 70 75 80	
Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn	
85 90 95	
Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu	
100 105 110	
Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val	
115 120 125	
Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu	
130 135 140	

Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
 145 150 155 160
 Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
 165 170 175
 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
 180 185 190
 Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
 195 200 205
 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
 210 215 220
 His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
 225 230 235 240
 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
 245 250 255
 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
 260 265 270
 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
 275 280 285
 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
 290 295 300
 Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
 305 310 315 320
 Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
 325 330 335
 Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln
 340 345 350
 Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile
 355 360 365
 Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu
 370 375 380
 Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu
 385 390 395 400
 Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro
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<211> 354

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<221> CDS

<222> (1)...(354)

<223> Insert identified by two-hybrid screening of a M.
musculus foetal cDNA library

<223> Insert identified by two-hybrid screening of a M.
musculus foetal cDNA library

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 His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu Lys Asp Leu Tyr
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acc gca gag tgt gag aag ctt cag agc att tac att gag gag gca gaa 96
 Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile Glu Glu Ala Glu
 20 25 30

aaa tat aaa act caa ctg caa gag cag ttt gac aac tta aac gcc gcc 144
 Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala Ala
 35 40 45

cat gag acc act aag ctt gag att gaa gct agc cac tcg gag aag gtg 192
 His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Val
 50 55 60

gaa ttg ctg aag aag acc tat gaa acc tcc ctt tca gaa atc aag aag 240
 Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser Glu Ile Lys Lys
 65 70 75 80

agc cat gag atg gag aag aag tca ctg gag gat ctg ctt aat gag aag 288
 Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu Leu Asn Glu Lys
 85 90 95

cag gaa tcg ctg gag aaa caa atc aat gat ctg aag agt gaa aac gat 336
 Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp
 100 105 110

gct tta aac gaa agg ttg 354
 Ala Leu Asn Glu Arg Leu
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<210> 6

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Insert identified by yeast two hybrid screening of
 a M. musculus fetal cDNA library

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His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu Lys Asp Leu Tyr
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 Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile Glu Glu Ala Glu
 20 25 30
 Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala Ala
 35 40 45
 His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Val
 50 55 60
 Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser Glu Ile Lys Lys

65		70		75		80
Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu Leu Asn Glu Lys						
	85		90		95	
Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp						
	100		105		110	
Ala Leu Asn Glu Arg Leu						
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<210> 7
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (293)...(1600)

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 cctgggggat ttttttcttc tatgcctctg tgggtggaatg acatttgctg tgtaggcac 180
 tttcctctga ctgtatttct tggccttgaa gactactgag tttaaaaaga cagtatgtga 240
 cagtccatgg aaattgcctc ttctgtgaaa tctcgccacc tgctccgaag ac atg ttg 298
 Met Leu
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ttg tct ccc aaa ttc tcc tta tcc acc att cac ata cga ctg acg gcc 346
 Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Ile Arg Leu Thr Ala
 5 10 15

aaa gga ttg ctt cga aac ctt cga ctt cct tca ggg ttt agg aga agc 394
 Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Phe Arg Arg Ser
 20 25 30

act gtt gtt ttc cac aca gtt gaa aag agc agg caa aag aat cct cga 442
 Thr Val Val Phe His Thr Val Glu Lys Ser Arg Gln Lys Asn Pro Arg
 35 40 45 50

agc tta tgt atc cag cca cag aca gct ccc gat gcg ctg ccc cct gag 490
 Ser Leu Cys Ile Gln Pro Gln Thr Ala Pro Asp Ala Leu Pro Pro Glu
 55 60 65

aaa aca ctt gaa ttg acg caa tat aaa aca aaa tgt gaa aac caa agt 538
 Lys Thr Leu Glu Leu Thr Gln Tyr Lys Thr Lys Cys Glu Asn Gln Ser
 70 75 80

gga ttt atc ctg cag ctc aag cag ctt ctt gcc tgt ggt aat acc aag 586
 Gly Phe Ile Leu Gln Leu Lys Gln Leu Leu Ala Cys Gly Asn Thr Lys
 85 90 95

ttt gag gca ttg aca gtt gtg att cag cac ctg ctg tct gag cgg gag 634
 Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu Arg Glu
 100 105 110

gaa	gca	ctg	aaa	caa	cac	aaa	acc	cta	tct	caa	gaa	ctt	gtt	aac	ctc	682
Glu	Ala	Leu	Lys	Gln	His	Lys	Thr	Leu	Ser	Gln	Glu	Leu	Val	Asn	Leu	
115					120					125					130	
cgg	gga	gag	cta	gtc	act	gct	tca	acc	acc	tgt	gag	aaa	tta	gaa	aaa	730
Arg	Gly	Glu	Leu	Val	Thr	Ala	Ser	Thr	Thr	Cys	Glu	Lys	Leu	Glu	Lys	
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Gln	Ala	Glu	Lys	Thr	Glu	Arg	Glu	Asn	Arg	Leu	Lys	Glu	Phe	Tyr	Thr	
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Arg	Glu	Tyr	Glu	Lys	Leu	Arg	Asp	Thr	Tyr	Ile	Glu	Glu	Ala	Glu	Lys	
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Tyr	Lys	Met	Gln	Leu	Gln	Glu	Gln	Phe	Asp	Asn	Leu	Asn	Ala	His	Glu	
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acc	tct	aag	ttg	gaa	att	gaa	gct	agc	cac	tca	gag	aaa	ctt	gaa	ttg	970
Thr	Ser	Lys	Leu	Glu	Ile	Glu	Ala	Ser	His	Ser	Glu	Lys	Leu	Glu	Leu	
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Leu	Lys	Lys	Ala	Tyr	Glu	Ala	Ser	Leu	Ser	Glu	Ile	Lys	Lys	Gly	His	
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Glu	Ile	Glu	Lys	Lys	Ser	Leu	Glu	Asp	Leu	Leu	Ser	Glu	Lys	Gln	Glu	
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Asn	Glu	Lys	Leu	Lys	Ser	Glu	Glu	Gln	Lys	Arg	Arg	Ala	Arg	Glu	Lys	
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Pro Glu Lys Thr Leu Glu Leu Thr Gln Tyr Lys Thr Lys Cys Glu Asn
65           70           75           80
Gln Ser Gly Phe Ile Leu Gln Leu Lys Gln Leu Leu Ala Cys Gly Asn
85           90           95
Thr Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
100          105          110
Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
115          120          125
Asn Leu Arg Gly Glu Leu Val Thr Ala Ser Thr Thr Cys Glu Lys Leu
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Tyr Thr Arg Glu Tyr Glu Lys Leu Arg Asp Thr Tyr Ile Glu Glu Ala
180          185          190
Glu Lys Tyr Lys Met Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala
195          200          205
His Glu Thr Ser Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Leu
210          215          220
Glu Leu Leu Lys Lys Ala Tyr Glu Ala Ser Leu Ser Glu Ile Lys Lys
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Gly His Glu Ile Glu Lys Lys Ser Leu Glu Asp Leu Leu Ser Glu Lys
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 290 295 300
 Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn Glu Lys Leu His
 305 310 315 320
 Gln Gln Asp Ile Lys Leu Met Lys Met Glu Lys Leu Val Asp Asn Asn
 325 330 335
 Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln Glu Asn Glu Glu
 340 345 350
 Leu Lys Ala Arg Met Asp Lys His Met Ala Ile Ser Arg Gln Leu Ser
 355 360 365
 Thr Glu Gln Ala Val Leu Gln Glu Ser Leu Glu Lys Glu Ser Lys Val
 370 375 380
 Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu Leu Trp Lys Leu His
 385 390 395 400
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 Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Phe Arg
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 aga agc act gtt gtt ttc cac aca gtt gaa aag agc agg caa aag aat 144
 Arg Ser Thr Val Val Phe His Thr Val Glu Lys Ser Arg Gln Lys Asn
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 cct cga agc tta tgt atc cag cca cag aca gct ccc gat gcg ctg ccc 192
 Pro Arg Ser Leu Cys Ile Gln Pro Gln Thr Ala Pro Asp Ala Leu Pro
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	115	120	125	
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Asn Leu Arg Gly Glu Leu Val Thr Ala Ser Thr Thr Cys Glu Lys Leu				
	130	135	140	
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Gly His Glu Ile Glu Lys Lys Ser Leu Glu Asp Leu Leu Ser Glu Lys				
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Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp				
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Tyr Thr Arg Glu Tyr Glu	Lys Leu Arg Asp Thr	Tyr Ile Glu Glu Ala
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34

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE-CNRS
 (B) STREET: 3 rue Michel-Ange
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 (E) COUNTRY: FRANCE
 (F) POSTAL CODE: 75794 PARIS Cedex 16

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 (C) CITY: Bagnolet
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 (F) POSTAL CODE: 93170

(A) NAME: NAHMIAS Clara
 (B) STREET: 4 rue Bailly
 (C) CITY: Paris
 (E) COUNTRY: FRANCE
 (F) POSTAL CODE: 75003

(A) NAME: STROSBERG Arthur Donny
 (B) STREET: 66 rue de Javel
 (C) CITY: Paris
 (E) COUNTRY: FRANCE
 (F) POSTAL CODE: 75015

(ii) TITLE OF THE INVENTION: NUCLEIC SEQUENCES ENCODING AN AT2
 RECEPTOR-INTERACTING PROTEIN (ATIP) AND THEIR APPLICATIONS

(iii) NUMBER OF SEQUENCES: 12

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1803 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 178..1500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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CAA AGT GGA TTC ATC CTG CAC CTC AGG CAG CTT CTT TCC CGT GGT AAC	465					
Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn						
85 90 95						
AAC AAG TTT GAA GCG CTG ACA GTT GTG ATC CAG CAC CTC CTG TCT GAG	513					
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Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu						
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165 170 175						
CTG AAG GAC TTA TAC ACC GCA GAG TGT GAG AAG CTT CAG AGC ATT TAC	753					
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180 185 190						

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Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp	
195 200 205	
AAC TTA AAC GCC GCC CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC	849
Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser	
210 215 220	
CAC TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT	897
His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu	
225 230 235 240	
TCA GAA ATC AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT	945
Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp	
245 250 255	
CTG CTT AAT GAG AAG CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG	993
Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu	
260 265 270	
AAG AGT GAA AAC GAT GCT TTA AAC GAA AGG TTG AAA TCA GAG GAG CAA	1041
Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln	
275 280 285	
AAG CAA CTG TCA AGA GAG AAG GCG AAT TCC AAA AAC CCT CAG GTC ATG	1089
Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met	
290 295 300	
TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG GCT GTG TTA GAG ATC AAG	1137
Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys	
305 310 315 320	
AAT GAG AAG CTG CAC CAG CAG GAC ATG AAG CTA ATG AAG ATG GAA AAG	1185
Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys	
325 330 335	
CTG GTG GAC AAT AAC ACA GCA TTG GTT GAC AAG CTG AAG CGA TTC CAG	1233
Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln	
340 345 350	
CAG GAA AAC GAG GAG TTA AAA GCT CGC ATG GAC AAA CAC ATG GCA ATT	1281
Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile	
355 360 365	
TCA AGG CAA CTT TCC ACC GAG CAG GCC GCG CTG CAA GAG TCC CTT GAG	1329
Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu	
370 375 380	
AAG GAG TCA AAG GTC AAC AAG AGA CTG TCC ATG GAG AAC GAG GAA CTT	1377
Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu	
385 390 395 400	
CTG TGG AAA CTG CAC AAC GGA GAC CTG TGC AGC CCC AAG AGA TCC CCC	1425
Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro	
405 410 415	

ACC TCC TCG GCC ATC CCT TTC CAG TCC CCC AGG AAT TCT GGT TCC TTC 1473
Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe
420 425 430

TCC AGC CCC AGC ATC TCA CCC AGA TGA CGGCTTCTGA ACGCAGGAGA 1520
Ser Ser Pro Ser Ile Ser Pro Arg *

435 440

CTCTCTGAAG GCACTGAGGT GCGCTTCTGC AGGACTGACC CTCTCATGGG AACTCGAGTT 1580

GCTGCGTTAG CTCTCTGGAA TATCCCCAGG ATATCGGGAG AGCAGCCGCC AACCGTATCA 1640

GCTACGTACG AATAGAGAGC TCCAATAGAA GACTTTTAAC TTGGTCCAAA AGCCTCCTCC 1700

AAAAACAGAT TTCGGAAC TGAGTGGACAT AGTTGCACAA AGCACTTACG GAACGAGGGA 1760

ACCTTGTTCT TTGCCTTCCT TCACCTAAGC ATAGGCTTTC CAG 1803

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu
1 5 10 15

Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg
20 25 30

Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn
35 40 45

Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser
50 55 60

Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser
65 70 75 80

Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn
85 90 95

Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
100 105 110

Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
115 120 125

Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu
130 135 140

Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
 145 150 155 160
 Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
 165 170 175
 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
 180 185 190
 Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
 195 200 205
 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
 210 215 220
 His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
 225 230 235 240
 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
 245 250 255
 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
 260 265 270
 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
 275 280 285
 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
 290 295 300
 Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
 305 310 315 320
 Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
 325 330 335
 Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln
 340 345 350
 Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile
 355 360 365
 Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu
 370 375 380
 Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu
 385 390 395 400
 Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro
 405 410 415
 Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe
 420 425 430
 Ser Ser Pro Ser Ile Ser Pro Arg *
 435 440

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATC CAC GTC CGC CTA	48
Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu	
445 450 455	
ACC GCC AAA GGA CTG CTT CGA AAC CTC CGG CTT CCT TCG GGG CTC AGG	96
Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg	
460 465 470	
AAA AAC ACT GTC ATT TTC CAC ACA GTT GAA AAG GGC AGG CAG AAG AAT	144
Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn	
CCC AGG AGC CTG TGC ATC CAG ACC CAG ACA GCT CCA GAT GTG CTG TCC	192
Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser	
TCC GAG AGA ACG CTT GAG TTG GCC CAA TAC AAG ACA AAA TGT GAA AGC	240
Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser	
CAA AGT GGA TTC ATC CTG CAC CTC AGG CAG CTT CTT TCC CGT GGT AAC	288
Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn	
AAC AAG TTT GAA GCG CTG ACA GTT GTG ATC CAG CAC CTC CTG TCT GAG	336
Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu	
CGG GAG GAA GCA CTG AAG CAA CAC AAA ACC CTC TCT CAA GAA CTT GTC	384
Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val	
AGC CTC CGG GGA GAG CTA GTT GCT GCT TCA AGC GCC TGT GAG AAG CTA	432
Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu	
GAA AAG GCT AGG GCT GAC TTA CAG ACA GCG TAT CAA GAA TTT GTC CAG	480
Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln	

AAA CTA AAC CAG CAG CAT CAG ACA GAC CGG ACG GAA CTG GAG AAC CGG Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg	528
CTG AAG GAC TTA TAC ACC GCA GAG TGT GAG AAG CTT CAG AGC ATT TAC Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr	576
ATT GAG GAG GCA GAA AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT GAC Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp	624
AAC TTA AAC GCC GCC CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser	672
CAC TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu	720
TCA GAA ATC AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp	768
CTG CTT AAT GAG AAG CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu	816
AAG AGT GAA AAC GAT GCT TTA AAC GAA AGG TTG AAA TCA GAG GAG CAA Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln	864
AAG CAA CTG TCA AGA GAG AAG GCG AAT TCC AAA AAC CCT CAG GTC ATG Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met	912
TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG GCT GTG TTA GAG ATC AAG Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys	960
AAT GAG AAG CTG CAC CAG CAG GAC ATG AAG CTA ATG AAG ATG GAA AAG Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys	1008
CTG GTG GAC AAT AAC ACA GCA TTG GTT GAC AAG CTG AAG CGA TTC CAG Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln	1056
CAG GAA AAC GAG GAG TTA AAA GCT CGC ATG GAC AAA CAC ATG GCA ATT Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile	1104
TCA AGG CAA CTT TCC ACC GAG CAG GCC GCG CTG CAA GAG TCC CTT GAG Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu	1152

AAG GAG TCA AAG GTC AAC AAG AGA CTG TCC ATG GAG AAC GAG GAA CTT 1200
 Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu

 CTG TGG AAA CTG CAC AAC GGA GAC CTG TGC AGC CCC AAG AGA TCC CCC 1248
 Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro

 ACC TCC TCG GCC ATC CCT TTC CAG TCC CCC AGG AAT TCT GGT TCC TTC 1296
 Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe

 TCC AGC CCC AGC ATC TCA CCC AGA TG A 1323
 Ser Ser Pro Ser Ile Ser Pro Arg

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 440 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu
 1 5 10 15
 Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg
 20 25 30
 Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn
 35 40 45
 Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser
 50 55 60
 Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser
 65 70 75 80
 Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn
 85 90 95
 Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
 100 105 110
 Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
 115 120 125
 Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu
 130 135 140
 Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
 145 150 155 160

Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
 165 170 175
 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
 180 185 190
 Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
 195 200 205
 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
 210 215 220
 His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
 225 230 235 240
 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
 245 250 255
 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
 260 265 270
 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
 275 280 285
 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
 290 295 300
 Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
 305 310 315 320
 Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
 325 330 335
 Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln
 340 345 350
 Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile
 355 360 365
 Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu
 370 375 380
 Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu
 385 390 395 400
 Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro
 405 410 415
 Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe
 420 425 430
 Ser Ser Pro Ser Ile Ser Pro Arg
 435 440

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CAT CAG ACA GAC CGG ACG GAA CTG GAG AAC CGG CTG AAG GAC TTA TAC	48
His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu Lys Asp Leu Tyr	
440 445 450	
ACC GCA GAG TGT GAG AAG CTT CAG AGC ATT TAC ATT GAG GAG GCA GAA	96
Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile Glu Glu Ala Glu	
455 460 465	
AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT GAC AAC TTA AAC GCC GCC	144
Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala Ala	
470 475 480	
CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC CAC TCG GAG AAG GTG	192
His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Val	
485 490 495 500	
GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT TCA GAA ATC AAG AAG	240
Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser Glu Ile Lys Lys	
505 510 515	
AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT CTG CTT AAT GAG AAG	288
Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu Leu Asn Glu Lys	
520 525 530	
CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG AAG AGT GAA AAC GAT	336
Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp	
535 540 545	
GCT TTA AAC GAA AGG TTG	354
Ala Leu Asn Glu Arg Leu	
550	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

11

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu Lys Asp Leu Tyr
 1 5 10 15
 Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile Glu Glu Ala Glu
 20 25 30
 Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala Ala
 35 40 45
 His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Val
 50 55 60
 Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser Glu Ile Lys Lys
 65 70 75 80
 Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu Leu Asn Glu Lys
 85 90 95
 Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp
 100 105 110
 Ala Leu Asn Glu Arg Leu
 115

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3742 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 293..1600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGTGTGATG TGGTTCAGAG GCAGCTTCTA GACCTGCAGG AGGGAGATTG TATTCAGAGG 60
 AAGAGCATCA TTTTGGCAAC ATCTGAAAGT GAAAACGGAA GCCAGAAACA CTTGGCCAGC 120
 CCTGGGGGAT TTTTTTCTTC TATGCCTCTG TGGTGAATG ACATTTGCTG TGTAGGCATC 180
 TTTCTCTGA CTGTATTTCT TGGCCTTGAA GAGTACTGAG TTTAAAAAGA CAGTATGTGA 240
 CAGTCCATGG AAATTGCCTC TTCTGTGAAA TCTCGCCACC TGCTCCGAAG AC ATG 295
 Met

TTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATT CAC ATA CGA CTG ACG Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Ile Arg Leu Thr	343
GCC AAA GGA TTG CTT CGA AAC CTT CGA CTT CCT TCA GGG TTT AGG AGA Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Phe Arg Arg	391
AGC ACT GTT GTT TTC CAC ACA GTT GAA AAG AGC AGG CAA AAG AAT CCT Ser Thr Val Val Phe His Thr Val Glu Lys Ser Arg Gln Lys Asn Pro	439
CGA AGC TTA TGT ATC CAG CCA CAG ACA GCT CCC GAT GCG CTG CCC CCT Arg Ser Leu Cys Ile Gln Pro Gln Thr Ala Pro Asp Ala Leu Pro Pro	487
GAG AAA ACA CTT GAA TTG ACG CAA TAT AAA ACA AAA TGT GAA AAC CAA Glu Lys Thr Leu Glu Leu Thr Gln Tyr Lys Thr Lys Cys Glu Asn Gln	535
AGT GGA TTT ATC CTG CAG CTC AAG CAG CTT CTT GCC TGT GGT AAT ACC Ser Gly Phe Ile Leu Gln Leu Lys Gln Leu Leu Ala Cys Gly Asn Thr	583
AAG TTT GAG GCA TTG ACA GTT GTG ATT CAG CAC CTG CTG TCT GAG CGG Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu Arg	631
GAG GAA GCA CTG AAA CAA CAC AAA ACC CTA TCT CAA GAA CTT GTT AAC Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val Asn	679
CTC CGG GGA GAG CTA GTC ACT GCT TCA ACC ACC TGT GAG AAA TTA GAA Leu Arg Gly Glu Leu Val Thr Ala Ser Thr Thr Cys Glu Lys Leu Glu	727
AAA GCC AGG AAT GAG TTA CAA ACA GTG TAT GAA GCA TTC GTC CAG CAG Lys Ala Arg Asn Glu Leu Gln Thr Val Tyr Glu Ala Phe Val Gln Gln	775
CAC CAG GCT GAA AAA ACA GAA CGA GAG AAT CGG CTT AAA GAG TTT TAC His Gln Ala Glu Lys Thr Glu Arg Glu Asn Arg Leu Lys Glu Phe Tyr	823
ACC AGG GAG TAT GAA AAG CTT CGG GAC ACT TAC ATT GAA GAA GCA GAG Thr Arg Glu Tyr Glu Lys Leu Arg Asp Thr Tyr Ile Glu Glu Ala Glu	871
AAG TAC AAA ATG CAA TTG CAA GAG CAG TTT GAC AAC TTA AAT GCG CAT Lys Tyr Lys Met Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala His	919
GAA ACC TCT AAG TTG GAA ATT GAA GCT AGC CAC TCA GAG AAA CTT GAA Glu Thr Ser Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Leu Glu	967
TTG CTA AAG AAG GCC TAT GAA GCC TCC CTT TCA GAA ATT AAG AAA GGC Leu Leu Lys Lys Ala Tyr Glu Ala Ser Leu Ser Glu Ile Lys Lys Gly	1015

CAT GAA ATA GAA AAG AAA TCG CTT GAA GAT TTA CTT TCT GAG AAG CAG His Glu Ile Glu Lys Lys Ser Leu Glu Asp Leu Leu Ser Glu Lys Gln	1063
GAA TCG CTA GAG AAG CAA ATC AAT GAT CTG AAG AGT GAA AAT GAT GCT Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp Ala	1111
TTA AAT GAA AAA TTG AAA TCA GAA GAA CAA AAA AGA AGA GCA AGA GAA Leu Asn Glu Lys Leu Lys Ser Glu Glu Gln Lys Arg Arg Ala Arg Glu	1159
AAA GCA AAT TTG AAA AAT CCT CAG ATC ATG TAT CTA GAA CAG GAG TTA Lys Ala Asn Leu Lys Asn Pro Gln Ile Met Tyr Leu Glu Gln Glu Leu	1207
GAA AGC CTG AAA GCT GTG TTA GAG ATC AAG AAT GAG AAA CTG CAT CAA Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn Glu Lys Leu His Gln	1255
CAG GAC ATC AAG TTA ATG AAA ATG GAG AAA CTG GTG GAC AAC AAC ACA Gln Asp Ile Lys Leu Met Lys Met Glu Lys Leu Val Asp Asn Asn Thr	1303
GCA TTG GTT GAC AAA TTG AAG CGT TTC CAG CAG GAG AAT GAA GAA TTG Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln Glu Asn Glu Glu Leu	1351
AAA GCT CGG ATG GAC AAG CAC ATG GCA ATC TCA AGG CAG CTT TCC ACG Lys Ala Arg Met Asp Lys His Met Ala Ile Ser Arg Gln Leu Ser Thr	1399
GAG CAG GCT GTT CTG CAA GAG TCG CTG GAG AAG GAG TCG AAA GTC AAC Glu Gln Ala Val Leu Gln Glu Ser Leu Glu Lys Glu Ser Lys Val Asn	1447
AAG CGA CTC TCT ATG GAA AAC GAG GAG CTT CTG TGG AAA CTG CAC AAT Lys Arg Leu Ser Met Glu Asn Glu Glu Leu Leu Trp Lys Leu His Asn	1495
GGG GAC CTG TGT AGC CCC AAG AGA TCC CCC ACA TCC TCC GCC ATC CCT Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro Thr Ser Ser Ala Ile Pro	1543
TTG CAG TCA CCA AGG AAT TCG GGC TCC TTC CCT AGC CCC AGC ATT TCA Leu Gln Ser Pro Arg Asn Ser Gly Ser Phe Pro Ser Pro Ser Ile Ser	1591
CCC AGA TGA CACGTCCCCA AAGTCCACAG ACTCTCTGAA AGCATTTTGA Pro Arg *	1640
TGCAGGTCTG CAGGACTGAC CCCAAGGAGG AACGTGGGCA CAAGAGGTAT ATCAGCACAC	1700
GTGTGATCAC CGTAGGTAAC TGGAGCGTCA CCACCGGCGG AATCGAGCTT CTGAGACTGG	1760

AAGTCTGGAG	GAAGACTTTT	GCCTCCGTCC	AAAAGATTCC	TCCAAAAAAA	GATTTAAAAA	1820
AAGATTTTCGG	CATCGACACG	GACGTTGTTG	CACAAAGCAC	TTAAAGAACG	AGAGCATCTT	1880
GTTTCATTGCC	TTTTTCACCT	AAGCATAAGG	GGAAAAACTC	TCAGGGCCCCT	ATTAAGATTT	1940
ATAACCTTTG	TAATGTTCTT	CACCACAGAC	ACCTTCTTGT	GAGTTTTCAG	TCTGACTGTG	2000
GGGGTGGGGG	GTGTGAATGA	AATGGATGTC	ACAGAGTGTC	ATGTGTCTGA	TGCAGCCTCC	2060
TCTGCTGTGT	ATTAAATGTC	AAAATCTGAA	TATATCTGGA	TATGTACTAA	TCAAATAATA	2120
ATCAATCAAT	CAGCATATAC	ATTTTCAGCCA	AAGCCATAGA	AGAAAAAGCA	ATAGTTGCTT	2180
GAATTATGAT	CATCTACCAC	CAACTCTGCT	CAGCCCTGTA	ACAGGGTAGG	GAGAGGGTAT	2240
AACAGGAAGA	GCTTTGACTT	GTCCCTGTCT	ATACATTCTC	TGTATCTTTT	GGGGGTAACT	2300
TCTTGGCAGT	TTTTCAGTGT	TCAGCCATGT	CAGTTGAAAC	TAGATTTTTT	TGTAGATTTT	2360
TTACTTACCC	ATGTGAGCCT	AACACTATCC	TGTAATTCAT	TTTCTCAGGC	TATGTGTAAA	2420
TGTAGAACCC	TAATTTTTCT	ATAAAAAAAC	AAACTAACTA	ACTGTGTAAA	GAAAGAAAAA	2480
GGGAAGTACC	AATGGGTTTT	TCCACCTTAT	TTTTACCTTT	GATCTACCCT	TGCAGATTTA	2540
ACCTGTCTTC	TTCCCTCCCA	TTATTCTCAT	TTTCCTTTTA	CCTTTCTCCA	CCATCCAGAG	2600
CCACAAAAGC	AAACCTTCTA	CCTCCTACCT	ACTTTTCTCT	GGGACAAGGA	TAAAGGAATA	2660
TGATTTTCCA	GAGCCCCAGA	GCCAGCTCAT	CTTCCAGGTG	CTGAAACCAC	TTTCCAAATA	2720
AACTAAAGCC	TGGATTTGAT	ATTACAAATT	TTGGGAAATC	TTAGAATAAA	GAACGAGAAC	2780
AAGGAAGTCA	TTGGCTAGTA	TAATTAAGAA	AGGTAGGATT	CAGTGCTTAC	CGATGATGCA	2840
GTACTIONGATA	GAAGAAAACA	GTCTGGGAGG	ATAGCGCTCA	TTTTTCAGTT	ACCCTTTAAG	2900
GAGTCCCTTT	GTCTTTGGGA	AAGTAGCAGA	ATGGTCCGCT	TCTTTCCCAT	GAGTGGAATA	2960
TGTGGCTTGT	CCAACCTCTC	TCCAGGTTGC	ATTTTCAGTT	CTTTCCAAAA	CTTATTACCT	3020
CCCCTAATCC	TGAGACTTTG	GAAAAGGTGG	AAGGAAGAAC	TGTTGCTTTA	TCTCCCCCTC	3080
CCTGCATGTG	TCAACATTGT	GATGTCAGTA	TTTACTAATC	TACATTTCAGT	GGCTGTACAA	3140
ATAACAGCTG	TAGTAAGAAG	AGATTTCAGGA	TGCTAGAGGT	GAATATTTGG	GTCATTTTACA	3200
TGTACACTAC	ATAGCAAGTT	GATACTCATG	TTGCATGTTT	TTTTAAATTA	GTGATTTTGT	3260
GTCTTAAGTC	TTTAACTTCC	AATACTTCAT	CATGTATGTA	ACCTTCCATG	TTTGCTTCTG	3320
ATAAATGGAA	ATGTAGGTTT	ACTGCCACTT	CATGAGATAT	CTCTGCTCAC	GCTTCCAAGT	3380
TGTTCTCAAT	GACATTAGCC	AAAGTTGGGT	TTGCCATTCA	TCCCCTAGGC	ATGGTAAATC	3440
TTGTGTTGTT	CCCTGCTGTC	CTCCGTATTA	CGTGACCGGC	AAATAAATCT	CATAGCAGTT	3500

AATATAAAAC ATCTTTGGAG GATGGGAGAG AACAGGAGGG AAGATGGGAA ACAAATAGA 3560
 GAATTCTTAA GATTTTGT TT AAACCAAATG TTTCATGTAG AATGCAAAT GTTGGCACGT 3620
 CAAAATATG AATGTGTAGA CAACTGTAGT TGTGCTCAGT TTGTAGTGAT GGGAAGTGTA 3680
 TTTTACTCTG ATCAAATAAA TAATGCTGGA ATACTCAAAA AAAAAAAAAA AAAAAAAAAA 3740
 AA 3742

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Ile Arg Leu
 1 5 10 15
 Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Phe Arg
 20 25 30
 Arg Ser Thr Val Val Phe His Thr Val Glu Lys Ser Arg Gln Lys Asn
 35 40 45
 Pro Arg Ser Leu Cys Ile Gln Pro Gln Thr Ala Pro Asp Ala Leu Pro
 50 55 60
 Pro Glu Lys Thr Leu Glu Leu Thr Gln Tyr Lys Thr Lys Cys Glu Asn
 65 70 75 80
 Gln Ser Gly Phe Ile Leu Gln Leu Lys Gln Leu Leu Ala Cys Gly Asn
 85 90 95
 Thr Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
 100 105 110
 Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
 115 120 125
 Asn Leu Arg Gly Glu Leu Val Thr Ala Ser Thr Thr Cys Glu Lys Leu
 130 135 140
 Glu Lys Ala Arg Asn Glu Leu Gln Thr Val Tyr Glu Ala Phe Val Gln
 145 150 155 160
 Gln His Gln Ala Glu Lys Thr Glu Arg Glu Asn Arg Leu Lys Glu Phe
 165 170 175
 Tyr Thr Arg Glu Tyr Glu Lys Leu Arg Asp Thr Tyr Ile Glu Glu Ala
 180 185 190

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Glu Lys Tyr Lys Met Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala
 195 200 205
 His Glu Thr Ser Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Leu
 210 215 220
 Glu Leu Leu Lys Lys Ala Tyr Glu Ala Ser Leu Ser Glu Ile Lys Lys
 225 230 235 240
 Gly His Glu Ile Glu Lys Lys Ser Leu Glu Asp Leu Leu Ser Glu Lys
 245 250 255
 Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp
 260 265 270
 Ala Leu Asn Glu Lys Leu Lys Ser Glu Glu Gln Lys Arg Arg Ala Arg
 275 280 285
 Glu Lys Ala Asn Leu Lys Asn Pro Gln Ile Met Tyr Leu Glu Gln Glu
 290 295 300
 Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn Glu Lys Leu His
 305 310 315 320
 Gln Gln Asp Ile Lys Leu Met Lys Met Glu Lys Leu Val Asp Asn Asn
 325 330 335
 Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln Glu Asn Glu Glu
 340 345 350
 Leu Lys Ala Arg Met Asp Lys His Met Ala Ile Ser Arg Gln Leu Ser
 355 360 365
 Thr Glu Gln Ala Val Leu Gln Glu Ser Leu Glu Lys Glu Ser Lys Val
 370 375 380
 Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu Leu Trp Lys Leu His
 385 390 395 400
 Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro Thr Ser Ser Ala Ile
 405 410 415
 Pro Leu Gln Ser Pro Arg Asn Ser Gly Ser Phe Pro Ser Pro Ser Ile
 420 425 430
 Ser Pro Arg *
 435

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1308 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGTTGTTGT CTCCCAAATT CTCCTTATCC ACCATTACACA TACGACTGAC GGCCAAAGGA	60
TTGCTTCGAA ACCTTCGACT TCCTTCAGGG TTTAGGAGAA GCACTGTTGT TTTCCACACA	120
GTTGAAAAGA GCAGGCAAAA GAATCCTCGA AGCTTATGTA TCCAGCCACA GACAGCTCCC	180
GATGCGCTGC CCCCTGAGAA AACACTTGAA TTGACGCAAT ATAAAACAAA ATGTGAAAAC	240
CAAAGTGGAT TTATCCTGCA GCTCAAGCAG CTTCTTGCCT GTGGTAATAC CAAGTTTGAG	300
GCATTGACAG TTGTGATTCA GCACCTGCTG TCTGAGCGGG AGGAAGCACT GAAACAACAC	360
AAAACCCTAT CTCAAGAACT TGTTAACCTC CGGGGAGAGC TAGTCACTGC TTCAACCACC	420
TGTGAGAAAT TAGAAAAAGC CAGGAATGAG TTACAAACAG TGTATGAAGC ATTCGTCCAG	480
CAGCACCAGG CTGAAAAAAC AGAACGAGAG AATCGGCTTA AAGAGTTTTA CACCAGGGAG	540
TATGAAAAGC TTCGGGACAC TTACATTGAA GAAGCAGAGA AGTACAAAAT GCAATTGCAA	600
GAGCAGTTTG ACAACTTAAA TGCGCATGAA ACCTCTAAGT TGGAAATTGA AGCTAGCCAC	660
TCAGAGAAAC TTGAATTGCT AAAGAAGGCC TATGAAGCCT CCCTTTCAGA AATTAAGAAA	720
GGCCATGAAA TAGAAAAGAA ATCGCTTGAA GATTTACTTT CTGAGAAGCA GGAATCGCTA	780
GAGAAGCAAA TCAATGATCT GAAGAGTGAA AATGATGCTT TAAATGAAAA ATTGAAATCA	840
GAAGAACAAA AAAGAAGAGC AAGAGAAAAA GCAAATTTGA AAAATCCTCA GATCATGTAT	900
CTAGAACAGG AGTTAGAAAAG CCTGAAAGCT GTGTTAGAGA TCAAGAAATGA GAAACTGCAT	960
CAACAGGACA TCAAGTTAAT GAAAATGGAG AAAGTGGTGG ACAACAACAC AGCATTGGTT	1020
GACAAATTGA AGCGTTTCCA GCAGGAGAAT GAAGAATTGA AAGCTCGGAT GGACAAGCAC	1080
ATGGCAATCT CAAGGCAGCT TTCCACGGAG CAGGCTGTTC TGCAAGAGTC GCTGGAGAAG	1140
GAGTCGAAAG TCAACAAGCG ACTCTCTATG GAAAACGAGG AGCTTCTGTG GAAACTGCAC	1200
AATGGGGACC TGTGTAGCCC CAAGAGATCC CCCACATCCT CCGCCATCCC TTTGCAGTCA	1260
CCAAGGAATT CGGGCTCCTT CCCTAGCCCC AGCATTTAC CCAGATGA	1308

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CAAGCGTTCT CTCGGAGGAC A

21

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGCGGATCCC AGACAGACCG GACGGAACTG GAG

33

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCGGAATTCA CTACAACCTT TCGTTTAAAG CATC

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